

Figure S1 Representative structures for shallow (left) and deep- (right) blocking conformations of ssDNA and its relative proximity to the hemolysin pore

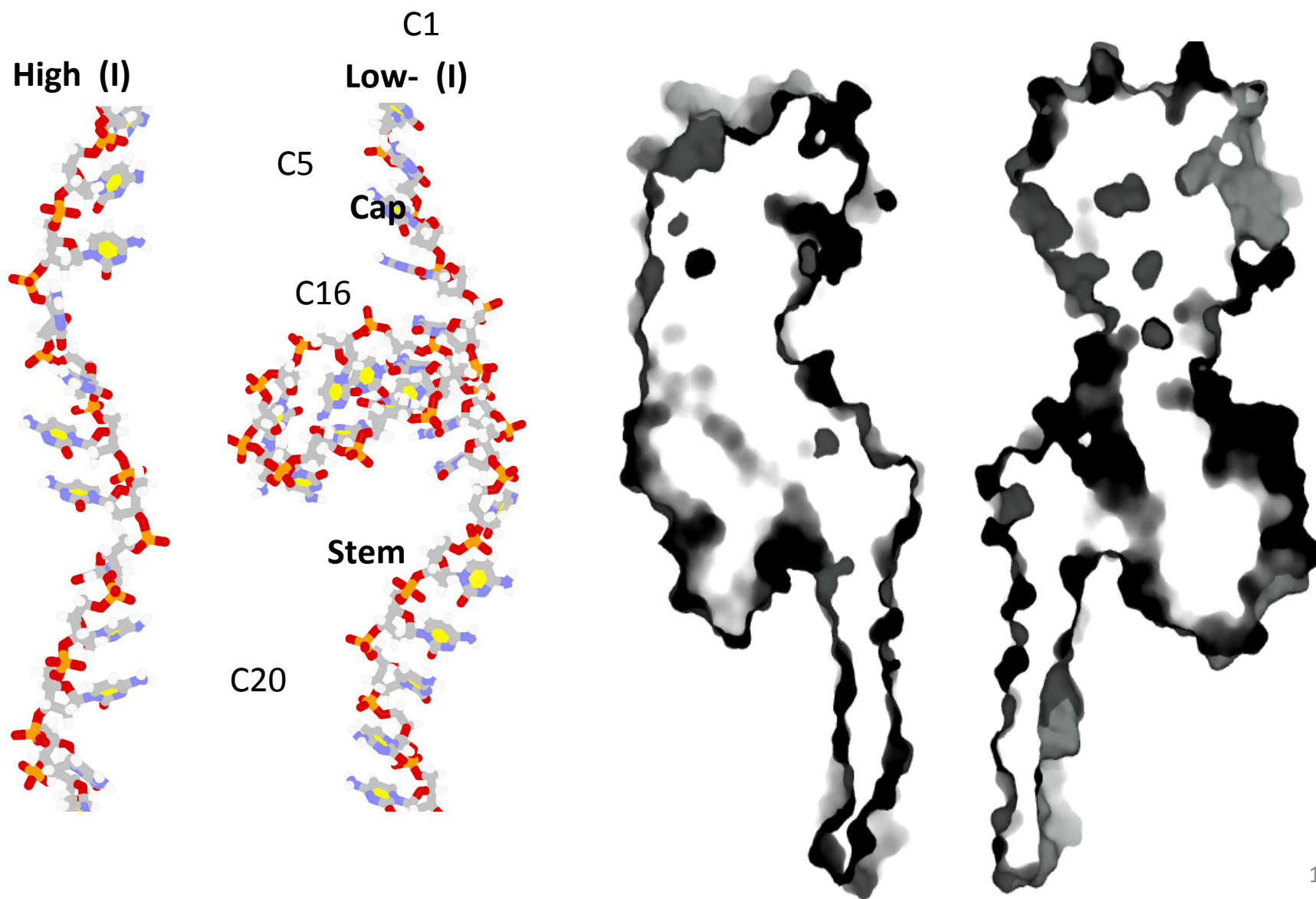


FIGURE S2: Time series of the mean square displacement (MSD) for tandems of nucleotides confined in the protein cap (left), first sensing (E111-K147, center) and second sensing zones (N121-N129, right), for five independent MD simulations with $V=600$ mV and a 1M concentration of KCl.

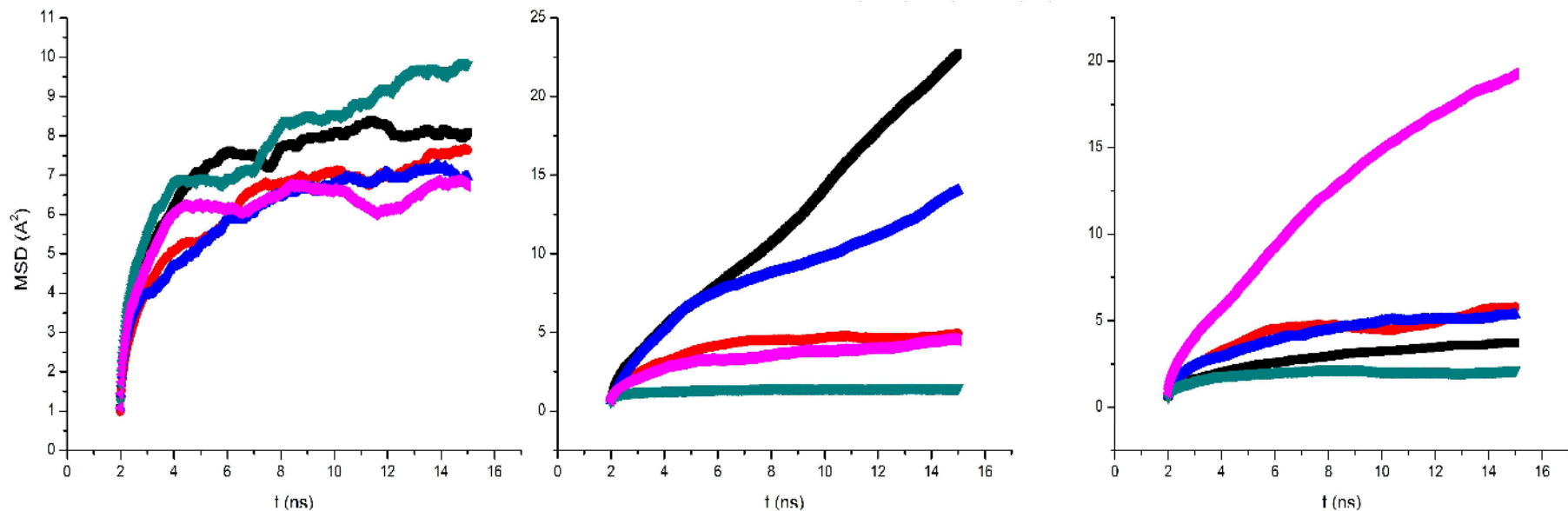


FIGURE S3: The water dipole orientation along the Z-axis from 200 ns equilibrium MD simulations for truncated system with poly(dC)₂₀ captured in the pore.

